Abstract

Mathematical models to describe in vivo and in vitro immunological response to infection in humans by HIV-1 have been of major concern due to the rich variety of parameters affecting its dynamics. In this paper, HIV-1 in vivo dynamics is studied to predict and describe its evolutions in presence of ARVs using delay differential equations. The delay is used to account for the latent period of time that elapsed between HIV – CD4+T cell binding (infection) and production of infectious virus from this host cell. The model uses four variables: healthy CD4+T-cells (T), infected CD4+T-cells (T*), infectious virus (VI) and non infectious virus (VN). Of importance is effect of time delay and drug efficacy on stability of disease free and endemic equilibrium points. Analytical results showed that DFE is stable for all > 0. On the other hand, there is a critical value of delay> 0, such that for all > , the EEP is stable but unstable for < . The critical value of delay is the bifurcation value where the HIV-1 in vivo dynamics undergoes a Hop f-bifurcation. This stability in both equilibria is achieved only if the drug efficacy 0 ≤ □ ≤ lis above a threshold value of. Numerical simulations show that this stability is achieved at the drug efficacy of = 0.59and time delay of = 0.65days. This ratifies the fact that if CD4+T cells remain inactive for long periods of time > the HIV-1 viral materials will not be reproduced, and the immune system together with treatment will have enough time to clear the viral materials in the blood and thus the EEP is maintain.